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IκB, NF-κB Regulation Model: Simulation Analysis of Small Number of Molecules

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Abstract

The regulation of IκB, NF-κB is of foremost interest in biology as the transcription factor NF-κB has multiple target genes. We have modeled a previously published model by Hoffmann et al. (2002) of IκB, NF-κB mathematically as discrete reaction systems. We have used stochastic algorithm to compare the results when there are large and small numbers of molecules available in a finite volume for each protein. Our results for small number of molecules show that with continuous presence of stimulation, nuclear NF-κB oscillates continuously in every individual cell rather than damping, which was observed in cell population results. This characteristic of the system is missed when averaged behavior is studied.

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